Evolutionary and Population Genetics of *Jasus* Species Inferred from Mitochondrial DNA

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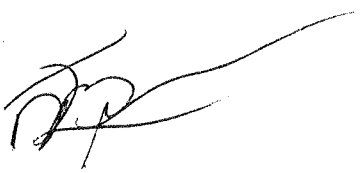
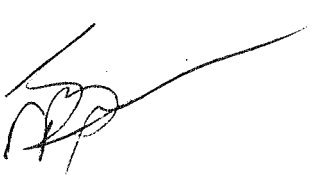
Declaration and Statement

I hereby declare that this thesis contains no material which has been accepted for the award of any degree or diploma in any university and that, to the best of my knowledge, this thesis contains no copy of previously published material except where due reference is made in the text.



D.J. Brasher
18 January 1994

The work reported in this thesis was carried out by D.J. Brasher under the supervision of Drs R.W.G. White and J.R. Ovenden using funds from a grant to Drs Ovenden and White from the Fishing Industry Research and Development Council (FIRDC). Most of the material in this thesis has already been published; references to the publications are given at the beginning of each of Chapters 3, 4 and 5. Mr. Brasher is the senior author on two of the papers (reported in Chapters 3 and 5); Dr Ovenden is the senior author on the the third paper (reported in Chapter 4). Mr Brasher carried out all of the practical work and the majority of the analyses for this latter paper. Dr Ovenden's seniority in the authorship list recognises her inception of the project, her success in obtaining the research funds and her supervisory and creative input.



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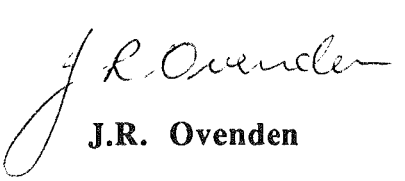

J.R. Ovenden

R.W.G. White

Summary

Restriction enzyme analysis of mtDNA extracted from antennal gland tissue was used to assess mtDNA variation within and between five nominal species of commercially important rock lobster, genus *Jasus*. Samples were collected from South Africa (*Jasus lalandii*, sample size=11), Vema Seamount in the South Atlantic Ocean (*J. tristani*, 8), Tasmania (*J. novaehollandiae*, 11), and New Zealand (*J. edwardsii*, 10; *J. verreauxi*, 9).

The generally high degree of intraspecific mtDNA nucleotide sequence diversity detected (0.33–0.99%) with six five- and six-base enzymes enabled high resolution assessment of species boundaries previously defined only by morphological criteria. Sequence diversity analysis failed to reveal significant mtDNA diversity between the *J. edwardsii* and *J. novaehollandiae* samples. Furthermore, phylogenetic reconstruction, using both phenetic and parsimony analysis of the restriction site data, did not partition mtDNA haplotypes into distinct Australian and New Zealand assemblages. These results suggest that Australian and New Zealand red rock lobster represent conspecific populations of *J. edwardsii*.

High sequence diversities separating *J. edwardsii*, *J. lalandii* and *J. tristani* (4.41–7.36%) indicates long-term reproductive isolation and provides confirmation of their specific status. The genome of *J. verreauxi* is highly distinct from the genomes of the other species (nucleotide sequence diversity: 14.92–16.67%), supporting the existence of *'lalandii'* and *'verreauxi'* groups within *Jasus*.

The topologies of trees generated by phylogenetic analyses grouped *J. edwardsii* and *J. lalandii* to the exclusion of *J. tristani;* however, further analysis indicated that the relationships of these species was essentially unresolved. Nevertheless, these results, when considered with knowledge of the current distributions of these species, do not support hypotheses for the evolution of *'lalandii'* group Jasus, which suggest a relatively recent divergence of *J. lalandii* and *J. tristani*. Instead, they give systematic validity to the grouping of *J. lalandii* with *J. edwardsii* as proposed by the existing taxonomy.

A restriction enzyme study of mtDNA variation in *J. edwardsii* was extended to include samples collected from widespread locales across southern Australia and from New Zealand. A total of 132 adult lobsters from 13 locales were analysed to address the possibility of population subdivision. Phenetic analysis failed to reveal geographic partitioning of mtDNA haplotypes. Despite collection locations being separated by large geographical distances, sequence diversity analysis between pairs of samples failed to conclusively detect population subdivision. Gene diversity analyses also failed to detect subdivision, even when samples were grouped into likely populations based on hydrological and environmental parameters. These results suggest that genetic homogeneity is maintained in this species by widespread dispersal of a long-lived, planktonic larval stage.

Analyses to detect population subdivision were also applied to 25 *J. verreauxi* collected from one Australian and two New Zealand locales. From the raw restriction site data, Australian and New Zealand haplotype assemblages were defined by two restriction sites, one confined to each country. Genetic differentiation between Australian and New Zealand *J. verreauxi* was also supported by gene diversity analysis. In contrast to the population study of *J. edwardsii,* these results suggest that larval exchange between adult populations across the Tasman Sea may be limited.

Acknowledgements

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